Listing of claims:

1. **(Previously presented)** A method for identifying a non-peptide compound that binds to a target, the method comprising:

a) forming a first library comprising a multiplicity of peptides;

b) selecting from the first library a family of peptides that bind to the target;

c) determining the amino acid sequence or sequences of the family of peptides that bind to the target, thereby generating a peptide motif;

d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif, wherein said multiplicity of non-peptide compounds are selected from the group consisting of peptide analogues, peptidomimetics and peptide derivatives;

e) selecting from the second library at least one non-peptide compound that binds to the target; and

f) determining the structure or structures of the at least one non-peptide compound that binds to the target;

thereby identifying a non-peptide compound that binds to the target.

2. **(Original)** The method of claim 1, wherein the first library is a phage display library.

3. **(Original)** The method of claim 1, wherein the first library is bound to a solid-support.

4. **(Original)** The method of claim 1, wherein the first library is an anchor library.

5. **(Original)** The method of claim 1, wherein the first library comprises at least about 10^6 peptides.

6. **(Original)** The method of claim 1, wherein the first library comprises at least about 10^9 peptides.

7. **(Original)** The method of claim 1, wherein the first library comprises at least about 10^{12} peptides.

8-9. **(Canceled)**

10. **(Original)** The method of claim 1, wherein the second library comprises at least one peptide derivative.

11. **(Original)** The method of claim 1, wherein the second library comprises at least one peptide analogue.

12. **(Original)** The method of claim 1, wherein the second library comprises at least one peptidomimetic.

13. **(Original)** The method of claim 1, wherein the second library comprises at least about 10^2 non-peptide compounds.

14. **(Original)** The method of claim 1, wherein the second library comprises at least about 10^4 non-peptide compounds.

15. **(Original)** The method of claim 1, wherein the second library comprises at least about 10^6 non-peptide compounds.

16. **(Original)** The method of claim 1, wherein step f) comprises analyzing the at least one non-peptide compound by a mass spectrometric method.

17. **(Original)** The method of claim 16, wherein the mass spectrometric method comprises tandem mass spectrometry.

18. **(Previously presented)** The method of claim 1, wherein the non-peptide compound that binds to a target has a binding affinity for the target of at least about 10^{-7} M.

19. **(Previously presented)** The method of claim 1, wherein the non-peptide compound that binds to a target has a binding affinity for the target of at least about 10^{-8} M.

20. **(Previously presented)** The method of claim 1, wherein the non-peptide compound that binds to a target has a binding affinity for the target of at least about 10^{-9} M.

21. **(Previously presented)** The method of claim 1, further comprising:

g) forming a third library comprising a multiplicity of non-peptide compounds designed based on the structure or structures of the non-peptide compound or compounds determined in step f), wherein said multiplicity of non-peptide compounds are selected from the group consisting of peptide analogues, peptidomimetics and peptide derivatives;

h) selecting from the third library at least one non-peptide compound that binds to the target; and

i) determining the structure or structures of the at least one non-peptide compound selected in step h);

thereby identifying a non-peptide compound that binds to the target.

22. **(Previously presented)** A method for identifying a non-peptide compound that binds to a target, the method comprising:

a) forming a first library comprising a multiplicity of peptides displayed on the surface of a bacteriophage;

b) selecting from the first library a family of peptides that bind to the target;

c) determining the sequence or sequences of the family of peptides that bind to the target, thereby generating a peptide motif;

d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif, wherein said multiplicity of non-peptide compounds are selected from the group consisting of peptide analogues, peptidomimetics and peptide derivatives;

e) selecting from the second library at least one non-peptide compound that binds to the target; and

f) determining the structure or structures of the at least one non-peptide compound that binds to the target by tandem mass spectrometry;

thereby identifying a non-peptide compound that binds to the target.

23. **(Previously presented)** A method for identifying a non-peptide compound that binds to a target, the method comprising:

a) forming a first library comprising an anchor library of a multiplicity of peptides;

b) selecting from the first library a family of peptides that bind to the target;

c) determining the sequence or sequences of the family of peptides that bind to the target, thereby generating a peptide motif;

d) forming a second library comprising a multiplicity of non-peptide compounds designed based on the peptide motif, wherein said multiplicity of non-peptide compounds are

selected from the group consisting of peptide analogues, peptidomimetics and peptide derivatives;

e) selecting from the second library at least one non-peptide compound that binds to the target; and

f) determining the structure or structures of the at least one non-peptide compound that binds to the target by tandem mass spectrometry;

thereby identifying a non-peptide compound that binds to the target.

24-34. **(Canceled)**